

WHAT IS CLAIMED IS:

1. A bioconversion process to produce 1,3-propanediol comprising contacting, under suitable conditions, a carbon substrate with a single microorganism having at least one gene capable of expressing a dehydratase enzyme.
2. A bioconversion process to produce 1,3-propanediol comprising contacting, under suitable conditions, glycerol with a single microorganism having at least one gene capable of expressing a dehydratase enzyme, the microorganism selected from the group consisting of members of the genera *Aspergillus*, *Saccharomyces*, *Zygosaccharomyces*, *Pichia*, *Kluyveromyces*, *Candida*, *Hansenula*, *Debaryomyces*, *Mucor*, *Torulopsis*, *Methylobacter*, *Salmonella*, *Bacillus*, *Streptomyces*, and *Pseudomonas*.
3. The process of Claim 1 wherein the gene encodes glycerol dehydratase and is isolated from the group consisting of members of the genera *Klebsiella*, *Lactobacillus*, *Enterobacter*, *Citrobacter*, *Pelobacter*, *Ilyobacter*, and *Clostridium*.
4. The process of Claim 1 wherein the gene encodes diol dehydratase and is isolated from the group consisting of members of the genera *Klebsiella* and *Salmonella*.
5. The process of Claim 1 wherein the dehydratase enzyme is a glycerol dehydratase enzyme or diol dehydratase enzyme.
6. The process of Claim 1 wherein the microorganism is transformed with at least one DNA fragment encoding dhaB1, dhaB2, and dhaB3 and /or dhaT whereby the organism expresses active dehydratase enzyme.
7. The process of Claim 1 wherein the microorganism is selected from the group consisting of members of the genera *Citrobacter*, *Enterobacter*, *Clostridium*, *Klebsiella*, *Aerobacter*, *Lactobacillus*, *Aspergillus*, *Saccharomyces*, *Zygosaccharomyces*, *Pichia*, *Kluyveromyces*, *Candida*, *Hansenula*, *Debaryomyces*, *Mucor*, *Torulopsis*, *Methylobacter*, *Escherichia*, *Salmonella*, *Bacillus*, *Streptomyces* and *Pseudomonas*.
8. The process of Claim 7 wherein the microorganism is selected from the group consisting of recombinant microorganisms transformed with either a gene encoding a glycerol dehydratase enzyme or a gene encoding a diol dehydratase enzyme and mutant microorganisms having phenotypes which enhance production of 1,3-propanediol.
9. The process of Claim 7 wherein the microorganism is selected from the group consisting of members of the genera *Klebsiella*, *Enterobacter*, and *Citrobacter*, or is recombinant *Escherichia*.

10. The process of Claim 9 wherein the microorganism is recombinant *E. coli*.

11. The process of Claim 8 wherein the microorganism is selected from the group consisting of recombinant *Streptomyces sp.*, *Bacillus sp.*, *Pseudomonas sp.*, *Saccharomyces sp.*, *Aspergillus sp.*, *Lactobacillus sp.*, and *Pichia sp.*, the recombinant microorganism transformed with at least one DNA fragment encoding dhaB1, dhaB2, and dhaB3 and /or dhaT whereby the organism expresses active dehydratase enzyme and the carbon substrate is a monosaccharide.

12. The process of Claim 11 wherein the microorganism is selected from the group consisting of recombinant *Saccharomyces cerevisiae*, *Bacillus subtilis*, *Pichia pastoris*, and *Bacillus licheniformis*, the recombinant microorganism transformed with at least one DNA fragment encoding dhaB1, dhaB2, and dhaB3 and /or dhaT whereby the organism expresses active dehydratase enzyme and the carbon substrate is a monosaccharide.

13. The process of Claims 1 or 10 wherein the microorganism is a recombinant *E. coli* containing a glycerol dehydratase gene from *Klebsiella pneumoniae*.

14. The process of Claim 1 wherein the carbon substrate has at least a single carbon atom, provided that the carbon substrate is other than glycerol or dihydroxyacetone.

15. The process of Claim 14 wherein the carbon substrate is selected from the group consisting of monosaccharides, oligosaccharides and polysaccharides.

16. The process of Claim 15 wherein the carbon substrate is glucose.

17. The process of Claim 14 wherein the carbon substrate is an alcohol.

18. The process of Claim 1 further comprising growing the microorganism in a medium prior to contacting it with the carbon substrate.

19. 1,3-propanediol produced by the process of Claims 1 or 15.

20. A cosmid of about 35 kb isolated from *Klebsiella pneumoniae* comprising the DNA fragment encoding an active glycerol dehydratase enzyme having the restriction enzyme digest in Figure 1, columns 1 and 2.

21. A transformed microorganism comprising a host microorganism and the cosmid of Claim 20.

22. The transformed microorganism of Claim 21 wherein the host microorganism is *E. coli*, the microorganism designated by ATCC Accession No. 69789.

23. A transformed microorganism comprising a host microorganism and a first DNA fragment isolated from *Klebsiella pneumoniae*, the first DNA fragment encoding an active glycerol dehydratase enzyme having the restriction enzyme

digest in Figure 1, columns 1 and 2, and at least one second DNA fragment isolated from *Klebsiella pneumoniae*, the second DNA fragment encoding an active functional protein other than a glycerol dehydratase enzyme.

24. A recombinant microorganism comprising a DNA fragment encoding  
5 dhaB1, dhaB2, dhaB3, and dhaT, and selected from the group consisting of  
recombinant *Pseudomonas sp.* identified as ATCC Accession No. 55760,  
recombinant *Pichia pastoris* identified as ATCC Accession No. 74363,  
recombinant *Saccharomyces cerevisiae* pMCK1.10/17(MH)#A identified as  
ATCC Accession No. 74370, recombinant *Bacillus subtilis* strain  
10 BG2864/pM27(Clone #1) identified as ATCC Accession No. 98050, recombinant  
*Streptomyces lividans* strain SL14-2 identified as ATCC Accession No. 98052,  
and recombinant *Aspergillus niger* strain TGR40-13 identified as ATCC  
Accession No. 74369.

25. A recombinant *Bacillus licheniformis* strain BG188/pM26 (Clone #8),  
15 comprising a DNA fragment encoding dhaB1, dhaB2, and dhaB3, and designated  
by ATCC Accession No. 98051.

26. A recombinant eucaryote microorganism expressing dehydratase  
enzyme.

27. The recombinant eucaryote microorganism of Claim 26 selected from  
20 the group consisting of yeast and filamentous fungi.

28. The process of Claim 1 further comprising recovering 1,3-propanediol.